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ABSTRACT BOOK

“There will be epidemics...”

EBOLA: WORLD GOES ON RED ALERT

-2014

Six Dead, 17 Sick From
Drug-Resistant TB

-2017

Panic as
1,500
Die of
Malaria

-1898

Spread of Spanish Flu Menaces War Production

-1918

Cholera Epidemic
in Yemen Now
Affects One
Million People

-2017

Charity to Help Fight
Malaria in Africa

-2010

Ebola Out of Control

-2014

Death Toll Growing as Influenza
Claims Many Score Victims

-1918

Success in Tests of Yellow
Fever Serum Reported

-1932

**Brace for
Dengue**

-2017

**Dengue Dengue
EVERYWHERE**

-2017

Officials: Texas Sees Growing
Number of Typhus Cases

-2017

**FDA Busts Fake
Malaria Medicines**

-2013

**ZIKA THREAT
ON OUR
DOORSTEP**

-2016

New Hope
for AIDS Drug

-1996

**DIPHTHERIA:
Why Is It Back?**

-2017

Zika Spreads Worldwide

-2016

**Island Declares State of Emergency
Over Zika Virus, Dengue Fever Outbreak**

-2016

**ASTMH Annual Meeting
Canceled Due to
Spanish Flu Outbreak**

-1918

**QUARANTINE WANTED
as Yellow Fever Spreads**

-1878

**An American
Plague:
Yellow Fever
Epidemic of 1793**

-2003

Been to an Ebola-affected country?
Stay away from ASTMH meeting, Louisiana says

-2014

**Malaria Cases
on the Rise in
Last 3 Years**

-2016

astmh.org

ajtmh.org

#TropMed18



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any given time increasing the possibility of malaria-arboviral co-infections. More studies are needed to establish the relationship between vectors of different diseases and impact of immunity in disease transmission.

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DRIVING FORCE AND IMPACT OF URBANIZATION ON THE ECOLOGY OF *Aedes* MOSQUITOES IN YELLOW FEVER AND DENGUE CO-ENDEMIC AREAS IN COTE D'IVOIRE

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Aedes mosquito-borne arboviruses have increasingly occurred in rural and urban settings of Africa. We explored the effect of urbanization on *Aedes* ecology along a rural-to-urban gradient in yellow fever (YF) and dengue (DEN) co-endemic areas in Cote d'Ivoire. *Aedes* eggs, larvae and adults were sampled using ovitraps, larval surveys and human-baited double-net traps in rural, suburban and urban areas from January 2013 to December 2014. *Aedes* breeding sites were characterized, and species identified. A total of 51,439 specimens of *Aedes* mosquitoes belonging to 20 species (*Ae. aegypti*, *Ae. africanus*, *Ae. albopictus*, *Ae. angustus*, *Ae. apicoargenteus*, *Ae. argenteopunctatus*, *Ae. dendrophilus*, *Ae. fraseri*, *Ae. furcifer*, *Ae. haworthi*, *Ae. lilii*, *Ae. longipalpis*, *Ae. luteocephalus*, *Ae. metallicus*, *Ae. opok*, *Ae. palpalis*, *Ae. stokesi*, *Ae. unilineatus*, *Ae. usambara* and *Ae. vittatus*) were sampled. The highest *Aedes* species richness was found in rural (18 species), followed by suburban (7 species) and urban (3 species) areas. Conversely, *Aedes* showed higher abundance in urban ($n = 51,439$; 50.7%) compared to suburban (32.6%) and rural (16.7%) areas. *Aedes*-positive breeding sites were more abundant in urban (2,136/3,374; 63.3%) than suburban (1,428/3,069; 46.5%) and rural (738/2,423; 30.5%) areas. Breeding sites were mainly industrial (i.e., tires, cans and water receptacles), traditional (i.e., clay-pots) and natural (i.e., tree holes and fruit husks) containers in urban, suburban and rural areas, respectively. *Ae. aegypti*, *Ae. dendrophilus*, and *Ae. vittatus* bit humans in rural (4.48 bites/person/day), while *Ae. aegypti* inflicted 99.7% of bites in urban (15.73 bites/person/day) areas. *Ae. aegypti* was the dominant species and displayed bimodal daily feeding cycles in all areas, with stronger magnitude in urban areas. In Cote d'Ivoire, urbanization shifts *Aedes* ecology by restricting of wild *Aedes* species in rural and favoring *Ae. aegypti* in urban areas. Data suggested that while *Aedes* wild species act as bridge vectors of YF and DEN viruses in rural, *Ae. aegypti* raises the risk of inter-human transmission of arboviral diseases in urban areas.

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SPATIAL RISK OF URBAN EXPOSURE TO *ANOPHELES* AND *Aedes* MOSQUITO BITES IN AFRICA USING SALIVARY ANTIBODY-BASED BIOMARKERS

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Urban settings often present low densities of mosquito vectors which do not allow to accurately assess the risk of arthropod-borne diseases based on entomological parameters. This study aims to evaluate the spatial risk of both malaria and arbovirus transmission in a northern urban area of Senegal, West-Africa, using antibody-based biomarkers of human exposure to *Anopheles* and *Aedes* mosquito bites. A cross-sectional

study was undertaken between August and September 2014 (rainy season) in four urban districts (UDs) of the city of Saint-Louis, Senegal: Leona (LEO), Ndioloffène (NDI), Guet Ndar (GND) and Pikine Sor Diagne (PSD). In each UD, dry blood spots were performed in 809 children aged 6-59 months and ELISA method was used to evaluate IgG antibody (Ab) responses to both gSG6-P1 (*Anopheles*) and Nterm-34kDa (*Aedes*) peptides of respective mosquito saliva. The median of IgG response levels to both gSG6-P1 and Nterm-34kDa salivary peptide varied significantly according to UD and were lower in LEO compared to PSD, GND and NDI ($p < 0.0001$). Heat maps of IgG responses to both salivary peptides indicated variations in the spatial distribution of the intensity of Ab responses inside UD. There were no hot spots of malaria transmission risk (areas with children presenting a high IgG intensity) in LEO. Hot spots of malaria were mainly located in the northern part of NDI and GND, and in the southern part of PSD. As for the risk of arbovirus transmission, there were no hot spots in LEO and PSD. Hot spots of arbovirus transmission risk were located in some patch in the north of NDI and were dispersed throughout the UD of GND. Our results demonstrate that hot spots of both malaria and arbovirus transmission risk actually exist in northern parts of NDI and GND. This highlights that a targeted fight against mosquitoes in these hot spots could be effective against all mosquito-borne diseases. Antibody-based biomarkers could then help national control programs to target and prioritize vector control strategies in areas with common risk of malaria and arbovirus transmission.

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LARVAL ENVIRONMENT INFLUENCES MICROBIOTA OF CONTAINER DWELLING MOSQUITOES

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Mosquitoes host a community of microbiota that influence their growth, survival and susceptibility to pathogens. These microbiota are known to vary markedly between individuals but our understanding of the factors that influence this variation is still limited. The aim of this study was to determine how the larval environment influences the microbiome of two container-dwelling mosquito species, *Aedes triseriatus* and *Ae. japonicus*. Larvae of the two mosquito species were sampled from tire and tree-hole habitats at South Farms and Trelease Woods study sites in Champaign, Illinois, and their microbiome characterized through MiSeq sequencing of the 16S rRNA gene. Approximately 66% of bacterial operational taxonomic units (OTUs) were shared between mosquito larvae and water samples from the larval environment. *Dysgonomomonas* and an unclassified genus from family *Comamonadaceae* were the dominant bacterial taxa in *Ae. triseriatus* larvae and water samples respectively, but no clear dominance of any bacterial taxa was observed in *Ae. japonicus* larvae. Overall, there was significantly higher number of OTUs observed and predicted in mosquito larval samples compared to water samples. Bacterial OTU richness was significantly higher in *Ae. japonicus* tire samples from both study sites compared to *Ae. triseriatus* tire and tree-hole samples from South Farms or water samples from South Farms. NMDs plots based on Bray-Curtis distances revealed a clear separation of *Ae. japonicus*, *Ae. triseriatus* and water samples indicating that the bacterial communities differed by sample type. The findings of this study reveal that *Ae. japonicus* and *Ae. triseriatus* harbor distinct bacterial communities some of which are likely acquired from the larval environment.

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HOST PREFERENCES AND ACTIVITY RHYTHMS OF *ANOPHELES* MOSQUITOES IN CAMBODIA

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